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TECH CENTER 1600/2900

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DATE: 05/20/2003
TIME: 17:26:37

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/848,909A
Input Set : A:\00742.060002.SEQLIST.TXT
Output Set: N:\CRF4\05202003\I848909A.raw

4 <110> APPLICANT: Collier, R. John
5 Sellman, Brett R.
7 <120> TITLE OF INVENTION: Compounds and Methods for the Treatment
8 and Prevention of Bacterial Infection
11 <130> FILE REFERENCE: 00742/060002
13 <140> CURRENT APPLICATION NUMBER: US 09/848,909A
14 <141> CURRENT FILING DATE: 2001-05-04
16 <150> PRIOR APPLICATION NUMBER: US 60/201,800
17 <151> PRIOR FILING DATE: 2000-05-04
19 <160> NUMBER OF SEQ ID NOS: 35
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 735
25 <212> TYPE: PRT
26 <213> ORGANISM: Bacillus anthracis
28 <400> SEQUENCE: 1
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30 1 5 10 15
31 Gln Gly Leu Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro
32 20 25 30
33 Met Val Val Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser
34 35 40 45
35 Glu Leu Glu Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile
36 50 55 60
37 Trp Ser Gly Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala
38 65 70 75 80
39 Thr Ser Ala Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val
40 85 90 95
41 Ile Asn Lys Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg
42 100 105 110
43 Leu Tyr Gln Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys
44 115 120 125
45 Gly Leu Asp Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu
46 130 135 140
47 Val Ile Ser Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser
48 145 150 155 160
49 Ser Asn Ser Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro
50 165 170 175
51 Asp Arg Asp Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr
52 180 185 190
53 Thr Val Asp Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser
54 195 200 205
55 Asn Ile His Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu

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56	210	215	220
57	Lys Trp Ser Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr		
58	225	230	235
59	Gly Arg Ile Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val		240
60	245	250	255
61	Ala Ala Tyr Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser		
62	260	265	270
63	Lys Asn Glu Asp Gln Ser Thr Gln Asn Thr Asp Ser Glu Thr Arg Thr		
64	275	280	285
65	Ile Ser Lys Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His		
66	290	295	300
67	Gly Asn Ala Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val		
68	305	310	315
69	Ser Ala Gly Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His		320
70	325	330	335
71	Ser Leu Ser Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu		
72	340	345	350
73	Asn Thr Ala Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn		
74	355	360	365
75	Thr Gly Thr Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val		
76	370	375	380
77	Leu Gly Lys Asn Gln Thr Leu Ala Thr Ile Lys Ala Ala Glu Asn Gln		
78	385	390	395
79	400		
80	Leu Ser Gln Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu		
81	405	410	415
82	Ala Pro Ile Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile		
83	420	425	430
84	Thr Met Asn Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu		
85	435	440	445
86	Arg Leu Asp Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe		
87	450	455	460
88	Glu Asn Gly Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val		
89	465	470	475
90	480		
91	Leu Pro Gln Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys		
92	485	490	495
93	91 Asp Leu Asn Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp		
94	500	505	510
95	93 Pro Leu Glu Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys		
96	515	520	525
97	94 525		
98	Ile Ala Phe Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly		
99	530	535	540
100	95 540		
101	97 Lys Asp Ile Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln		
102	545	550	555
103	98 555		
104	Asn Ile Lys Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr		
105	565	570	575
106	100 575		
107	Val Leu Asp Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg		
108	580	585	590
109	103 Asp Lys Arg Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp		
110	595	600	605

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105 Glu Ser Val Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr
106 610 615 620
107 Glu Gly Leu Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser
108 625 630 635 640
109 Gly Tyr Ile Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile
110 645 650 655
111 Asn Asp Arg Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly
112 660 665 670
113 Lys Thr Phe Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr
114 675 680 685
115 Ile Ser Asn Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu
116 690 695 700
117 Asn Thr Ile Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly
118 705 710 715 720
119 Ile Lys Lys Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
120 725 730 735
123 <210> SEQ ID NO: 2
124 <211> LENGTH: 735
125 <212> TYPE: PRT
126 <213> ORGANISM: Bacillus anthracis
128 <400> SEQUENCE: 2
129 Glu Val Lys Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser
130 1 5 10 15
131 Gln Gly Leu Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro
132 20 25 30
133 Met Val Val Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser
134 35 40 45
135 Glu Leu Glu Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile
136 50 55 60
137 Trp Ser Gly Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala
138 65 70 75 80
139 Thr Ser Ala Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val
140 85 90 95
141 Ile Asn Lys Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg
142 100 105 110
143 Leu Tyr Gln Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys
144 115 120 125
145 Gly Leu Asp Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu
146 130 135 140
147 Val Ile Ser Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser
148 145 150 155 160
149 Ser Asn Ser Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro
150 165 170 175
151 Asp-Arg-Asp-Asn-Asp-Gly-Ile-Pro-Asp-Ser-Leu-Glu-Val-Glu-Gly-Tyr
152 180 185 190
153 Thr Val Asp Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser
154 195 200 205
155 Asn Ile His Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu
156 210 215 220

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157 Lys Trp Ser Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr
 158 225 230 235 240
 159 Gly Arg Ile Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val
 160 245 250 255
 161 Ala Ala Tyr Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser
 162 260 265 270
 163 Lys Asn Glu Asp Gln Ser Thr Gln Asn Thr Asp Ser Glu Thr Arg Thr
 164 275 280 285
 165 Ile Ser Lys Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His
 166 290 295 300
 167 Gly Asn Ala Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val
 168 305 310 315 320
 169 Ser Ala Gly Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His
 170 325 330 335
 171 Ser Leu Ser Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu
 172 340 345 350
 173 Asn Thr Ala Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn
 174 355 360 365
 175 Thr Gly Thr Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val
 176 370 375 380
 177 Leu Gly Lys Asn Gln Thr Leu Ala Thr Ile Lys Ala Asp Glu Asn Gln
 178 385 390 395 400
 179 Leu Ser Gln Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu
 180 405 410 415
 181 Ala Pro Ile Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile
 182 420 425 430
 183 Thr Met Asn Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu
 184 435 440 445
 185 Arg Leu Asp Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe
 186 450 455 460
 187 Glu Asn Gly Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val
 188 465 470 475 480
 189 Leu Pro Gln Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys
 190 485 490 495
 191 Asp Leu Asn Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp
 192 500 505 510
 193 Pro Leu Glu Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys
 194 515 520 525
 195 Ile Ala Phe Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly
 196 530 535 540
 197 Lys Asp Ile Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln
 198 545 550 555 560
 199 Asn Ile Lys Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr
 200 565 570 575
 201 Val Leu Asp Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg
 202 580 585 590
 203 Asp Lys Arg Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp
 204 595 600 605
 205 Glu Ser Val Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr

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206 610 615 620
 207 Glu Gly Leu Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser
 208 625 630 635 640
 209 Gly Tyr Ile Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile
 210 645 650 655
 211 Asn Asp Arg Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly
 212 660 665 670
 213 Lys Thr Phe Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr
 214 675 680 685
 215 Ile Ser Asn Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu
 216 690 695 700
 217 Asn Thr Ile Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly
 218 705 710 715 720
 219 Ile Lys Lys Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
 220 725 730 735
 223 <210> SEQ ID NO: 3
 224 <211> LENGTH: 735
 225 <212> TYPE: PRT
 226 <213> ORGANISM: Bacillus anthracis
 228 <400> SEQUENCE: 3
 229 Glu Val Lys Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser
 230 1 5 10 15
 231 Gln Gly Leu Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro
 232 20 25 30
 233 Met Val Val Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser
 234 35 40 45
 235 Glu Leu Glu Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile
 236 50 55 60
 237 Trp Ser Gly Phe Ile Lys Val Lys Ser Asp Glu Tyr Thr Phe Ala
 238 65 70 75 80
 239 Thr Ser Ala Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val
 240 85 90 95
 241 Ile Asn Lys Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg
 242 100 105 110
 243 Leu Tyr Gln Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys
 244 115 120 125
 245 Gly Leu Asp Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu
 246 130 135 140
 247 Val Ile Ser Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser
 248 145 150 155 160
 249 Ser Asn Ser Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro
 250 165 170 175
 251 Asp Arg Asp Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr
 252 180 185 190
 253 Thr Val Asp Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser
 254 195 200 205
 255 Asn Ile His Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu
 256 210 215 220
 257 Lys Trp Ser Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:19; Xaa Pos. 397
Seq#:23; Xaa Pos. 427